

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/SS3,431B  
Source: IFW16  
Date Processed by STIC: 1-5-05

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 01/05/2005

PATENT APPLICATION: US/09/553,431B

TIME: 15:03:50

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Output Set: N:\CRF4\01052005\I553431B.raw

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3 <110> APPLICANT: Osteryoung, Katherine W.
5 <120> TITLE OF INVENTION: Manipulation of Min Genes in Plants
7 <130> FILE REFERENCE: 920905.90041
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/553,431B
C--> 10 <141> CURRENT FILING DATE: 2000-04-19
12 <150> PRIOR APPLICATION NUMBER: 60/130,403
13 <151> PRIOR FILING DATE: 1999-04-19
15 <160> NUMBER OF SEQ ID NOS: 12
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 978
21 <212> TYPE: DNA
22 <213> ORGANISM: Prototheca wickerhamii
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25 <221> NAME/KEY: CDS
26 <222> LOCATION: (1)..(978)
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31 1 5 10 15
33 cca tca tct ctc tca caa aag act cta ata tct tca cca aga ttc gtc 96
34 Pro Ser Ser Leu Ser Gln Lys Thr Leu Ile Ser Ser Pro Arg Phe Val
35 20 25 30
37 aat aac cct agc aga cgg agt cca ata cga tcc gtt ctt caa ttt aat 144
38 Asn Asn Pro Ser Arg Arg Ser Pro Ile Arg Ser Val Leu Gln Phe Asn
39 35 40 45
41 cgc aaa ccg gaa ctc gcc gga gaa acg ccg cgt atc gtc gtt atc acc 192
42 Arg Lys Pro Glu Leu Ala Gly Glu Thr Pro Arg Ile Val Val Ile Thr
43 50 55 60
45 tcc gga aaa ggc ggt gtt gga aag acg aca acc acc gca aat gtc ggt 240
46 Ser Gly Lys Gly Gly Val Gly Lys Thr Thr Thr Thr Ala Asn Val Gly
47 65 70 75 80
49 ctc tct ctc gct cgt tac ggt ttc tca gtt gtc gcc att gac gcc gac 288
50 Leu Ser Leu Ala Arg Tyr Gly Phe Ser Val Val Ala Ile Asp Ala Asp
51 85 90 95
53 ctt ggt ctc cgt aac ctc gat ctc ctc cta ggg tta gag aat cga gtc 336
54 Leu Gly Leu Arg Asn Leu Asp Leu Leu Leu Gly Leu Glu Asn Arg Val
55 100 105 110
57 aat tac act tgc gtc gag gtt ata aac gga gat tgt cgt ctc gat caa 384
58 Asn Tyr Thr Cys Val Glu Val Ile Asn Gly Asp Cys Arg Leu Asp Gln
59 115 120 125
61 gct ctg gta cgt gat aag cgt tgg tcg aat ttc gaa ttg cta tgt ata 432
62 Ala Leu Val Arg Asp Lys Arg Trp Ser Asn Phe Glu Leu Leu Cys Ile

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65 tct aaa cct aga tcg aaa ctt ccg atg gga ttt ggt ggt aaa gca ttg 480
66 Ser Lys Pro Arg Ser Lys Leu Pro Met Gly Phe Gly Gly Lys Ala Leu
67 145      150      155      160
69 gaa tgg ctt gtg gat gcg ttg aaa act aga ccg gaa ggt tca ccg gat 528
70 Glu Trp Leu Val Asp Ala Leu Lys Thr Arg Pro Glu Gly Ser Pro Asp
71      165      170      175
73 ttc atc atc atc gat tgt cct gca gga atc gat gcc gga ttc ata acc 576
74 Phe Ile Ile Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe Ile Thr
75      180      185      190
77 gcc att act ccg gcg aat gaa gca gtt ctg gta aca act ccg gat ata 624
78 Ala Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro Asp Ile
79      195      200      205
81 aca gcg tta agg gat gct gat agg gtt acg ggt ttg tta gaa tgc gat 672
82 Thr Ala Leu Arg Asp Ala Asp Arg Val Thr Gly Leu Leu Glu Cys Asp
83      210      215      220
85 gga atc aga gat ata aag atg att gtg aac aga gtg aga act gat atg 720
86 Gly Ile Arg Asp Ile Lys Met Ile Val Asn Arg Val Arg Thr Asp Met
87 225      230      235      240
89 att aaa gga gag gat atg atg tca gtg tta gat gtg cag gag atg ttg 768
90 Ile Lys Gly Glu Asp Met Met Ser Val Leu Asp Val Gln Glu Met Leu
91      245      250      255
93 gga ttg tca ttg ctt ggt gta att cct gaa gat tct gag gtt att cga 816
94 Gly Leu Ser Leu Leu Gly Val Ile Pro Glu Asp Ser Glu Val Ile Arg
95      260      265      270
97 agc acg aat cga ggg ttt ccg ctt gtt ctg aat aag cct acg ctt 864
98 Ser Thr Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Pro Thr Leu
99      275      280      285
101 gcg gga ttg gcg ttt gag cag gcg gct tgg aga ctc gtt gag caa gat 912
102 Ala Gly Leu Ala Phe Glu Gln Ala Ala Trp Arg Leu Val Glu Gln Asp
103      290      295      300
105 agt atg aag gct gtt atg gtg gag gaa gaa cct aag aaa cgt ggc ttc 960
106 Ser Met Lys Ala Val Met Val Glu Glu Glu Pro Lys Lys Arg Gly Phe
107 305      310      315      320
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110 Phe Ser Phe Phe Gly Gly
111      325
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116 <212> TYPE: PRT
117 <213> ORGANISM: Prototheca wickerhamii
119 <400> SEQUENCE: 2
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123 Pro Ser Ser Leu Ser Gln Lys Thr Leu Ile Ser Ser Pro Arg Phe Val
124      20      25      30
126 Asn Asn Pro Ser Arg Arg Ser Pro Ile Arg Ser Val Leu Gln Phe Asn
127      35      40      45
129 Arg Lys Pro Glu Leu Ala Gly Glu Thr Pro Arg Ile Val Val Ile Thr

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130      50      55      60
132 Ser Gly Lys Gly Gly Val Gly Lys Thr Thr Thr Thr Ala Asn Val Gly
133 65      70      75      80
135 Leu Ser Leu Ala Arg Tyr Gly Phe Ser Val Val Ala Ile Asp Ala Asp
136      85      90      95
138 Leu Gly Leu Arg Asn Leu Asp Leu Leu Gly Leu Glu Asn Arg Val
139      100      105      110
141 Asn Tyr Thr Cys Val Glu Val Ile Asn Gly Asp Cys Arg Leu Asp Gln
142      115      120      125
144 Ala Leu Val Arg Asp Lys Arg Trp Ser Asn Phe Glu Leu Leu Cys Ile
145      130      135      140
147 Ser Lys Pro Arg Ser Lys Leu Pro Met Gly Phe Gly Gly Lys Ala Leu
148 145      150      155      160
150 Glu Trp Leu Val Asp Ala Leu Lys Thr Arg Pro Glu Gly Ser Pro Asp
151      165      170      175
153 Phe Ile Ile Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe Ile Thr
154      180      185      190
156 Ala Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro Asp Ile
157      195      200      205
159 Thr Ala Leu Arg Asp Ala Asp Arg Val Thr Gly Leu Leu Glu Cys Asp
160      210      215      220
162 Gly Ile Arg Asp Ile Lys Met Ile Val Asn Arg Val Arg Thr Asp Met
163 225      230      235      240
165 Ile Lys Gly Glu Asp Met Met Ser Val Leu Asp Val Gln Glu Met Leu
166      245      250      255
168 Gly Leu Ser Leu Leu Gly Val Ile Pro Glu Asp Ser Glu Val Ile Arg
169      260      265      270
171 Ser Thr Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Pro Thr Leu
172      275      280      285
174 Ala Gly Leu Ala Phe Glu Gln Ala Ala Trp Arg Leu Val Glu Gln Asp
175      290      295      300
177 Ser Met Lys Ala Val Met Val Glu Glu Glu Pro Lys Lys Arg Gly Phe
178 305      310      315      320
180 Phe Ser Phe Phe Gly Gly
181      325
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186 <211> LENGTH: 1182
187 <212> TYPE: DNA
188 <213> ORGANISM: Tagetes erecta
190 <220> FEATURE:
191 <221> NAME/KEY: CDS
192 <222> LOCATION: (50)..(934)
194 <400> SEQUENCE: 3
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196      Met Thr Ser
197      1
199 ctg agg ttt cta aca gaa ccc tca ctt gta tgc tca tcc act ttc ccc 106
200 Leu Arg Phe Leu Thr Glu Pro Ser Leu Val Cys Ser Ser Thr Phe Pro
201      5      10      15

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203 aca ttc aat ccc cta cac aaa acc cta act aaa cca aca cca aaa ccc 154
204 Thr Phe Asn Pro Leu His Lys Thr Leu Thr Lys Pro Thr Pro Lys Pro
205 20 25 30 35
207 tac cca aag cca cca cca att cgc tcc gtc ctt caa tac aat cgc aaa 202
208 Tyr Pro Lys Pro Pro Pro Ile Arg Ser Val Leu Gln Tyr Asn Arg Lys
209 40 45 50
211 cca gag ctc gcc gga gac act cca cga gtc gtc gca atc gac gcc gac 250
212 Pro Glu Leu Ala Gly Asp Thr Pro Arg Val Val Ala Ile Asp Ala Asp
213 55 60 65
215 gtt ggt cta cgt aac ctc gat ctt ctt ctc ggt ctc gaa aac cgc gtc 298
216 Val Gly Leu Arg Asn Leu Asp Leu Leu Leu Gly Leu Glu Asn Arg Val
217 70 75 80
219 aat tac acc gtc gtt gaa gtt ctc aac ggc gat tgc aga ctc gac caa 346
220 Asn Tyr Thr Val Val Glu Val Leu Asn Gly Asp Cys Arg Leu Asp Gln
221 85 90 95
223 gcc cta gtt cgt gat aaa cgc tgg tca aat ttc gaa ttg ctt tgt att 394
224 Ala Leu Val Arg Asp Lys Arg Trp Ser Asn Phe Glu Leu Leu Cys Ile
225 100 105 110 115
227 tca aaa cct agg tca aaa ttg cct tta gga ttt ggg gga aaa gct tta 442
228 Ser Lys Pro Arg Ser Lys Leu Pro Leu Gly Phe Gly Gly Lys Ala Leu
229 120 125 130
231 gtt tgg ctt gat gca tta aaa gat agg caa gaa ggt tgc ccg gat ttt 490
232 Val Trp Leu Asp Ala Leu Lys Asp Arg Gln Glu Gly Cys Pro Asp Phe
233 135 140 145
235 ata ctt ata gat tgt cct gca ggt att gat gcc ggg ttc ata acc gcc 538
236 Ile Leu Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe Ile Thr Ala
237 150 155 160
239 att aca ccg gct aac gaa gcc gta tta gtt aca aca cct gat att act 586
240 Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro Asp Ile Thr
241 165 170 175
243 gca ttg aga gat gca gat aga gtt aca ggc ttg ctt gaa tgt gat gga 634
244 Ala Leu Arg Asp Ala Asp Arg Val Thr Gly Leu Leu Glu Cys Asp Gly
245 180 185 190 195
247 att agg gat att aaa atg att gtg aac aga gtt aga act gat ttg ata 682
248 Ile Arg Asp Ile Lys Met Ile Val Asn Arg Val Arg Thr Asp Leu Ile
249 200 205 210
251 agg ggt gaa gat atg atg tca gtt ctt gat gtt caa gag atg ttg gga 730
252 Arg Gly Glu Asp Met Met Ser Val Leu Asp Val Gln Glu Met Leu Gly
253 215 220 225
255 ttg tca ttg ttg agt gat acc cga gga ttc gaa gtg att cgg agt acg 778
256 Leu Ser Leu Leu Ser Asp Thr Arg Gly Phe Glu Val Ile Arg Ser Thr
257 230 235 240
259 aat aga ggg ttt ccg ctt gtg ttg aac aag cct ccg act tta gca gga 826
260 Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Pro Thr Leu Ala Gly
261 245 250 255
263 ttg gca ttt gag cag gct gct tgg aga ttg gtt gag caa gat agc atg 874
264 Leu Ala Phe Glu Gln Ala Ala Trp Arg Leu Val Glu Gln Asp Ser Met
265 260 265 270 275
267 aag gct gtg atg gtg gag gaa gaa cct aaa aag agg gga ttt ttc tcg 922

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## RAW SEQUENCE LISTING

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Input Set : A:\Un900411.app

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268 Lys Ala Val Met Val Glu Glu Glu Pro Lys Lys Arg Gly Phe Phe Ser
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271 ttt ttt gga ggt tagtgatcga attcgttgaa tcgttgagtt gggtttgttt 974
272 Phe Phe Gly Gly
273      295
275 tgggtggagaa atgtgtcttg tttgttcattg taggagctgc tatgtgtcac ttgaaatggt 1034
277 atgtgtacag taagctgata aggattgttt taattcagtt ttcagagaga aaattagaat 1094
279 tgtagcaact tttcatttga tcaattcaat tgtatttctt tggttcagtg atgaattttt 1154
281 actcaaaatc aaaaaaaaaa aaaaaaaaaa 1182
284 <210> SEQ ID NO: 4
285 <211> LENGTH: 295
286 <212> TYPE: PRT
287 <213> ORGANISM: Tagetes erecta
289 <400> SEQUENCE: 4
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294 20 25 30
296 Pro Lys Pro Tyr Pro Lys Pro Pro Pro Ile Arg Ser Val Leu Gln Tyr
297 35 40 45
299 Asn Arg Lys Pro Glu Leu Ala Gly Asp Thr Pro Arg Val Val Ala Ile
300 50 55 60
302 Asp Ala Asp Val Gly Leu Arg Asn Leu Asp Leu Leu Gly Leu Glu
303 65 70 75 80
305 Asn Arg Val Asn Tyr Thr Val Val Glu Val Leu Asn Gly Asp Cys Arg
306 85 90 95
308 Leu Asp Gln Ala Leu Val Arg Asp Lys Arg Trp Ser Asn Phe Glu Leu
309 100 105 110
311 Leu Cys Ile Ser Lys Pro Arg Ser Lys Leu Pro Leu Gly Phe Gly Gly
312 115 120 125
314 Lys Ala Leu Val Trp Leu Asp Ala Leu Lys Asp Arg Gln Glu Gly Cys
315 130 135 140
317 Pro Asp Phe Ile Leu Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe
318 145 150 155 160
320 Ile Thr Ala Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro
321 165 170 175
323 Asp Ile Thr Ala Leu Arg Asp Ala Asp Arg Val Thr Gly Leu Leu Glu
324 180 185 190
326 Cys Asp Gly Ile Arg Asp Ile Lys Met Ile Val Asn Arg Val Arg Thr
327 195 200 205
329 Asp Leu Ile Arg Gly Glu Asp Met Met Ser Val Leu Asp Val Gln Glu
330 210 215 220
332 Met Leu Gly Leu Ser Leu Leu Ser Asp Thr Arg Gly Phe Glu Val Ile
333 225 230 235 240
335 Arg Ser Thr Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Pro Thr
336 245 250 255
338 Leu Ala Gly Leu Ala Phe Glu Gln Ala Ala Trp Arg Leu Val Glu Gln
339 260 265 270
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**VERIFICATION SUMMARY**

DATE: 01/05/2005

PATENT APPLICATION: US/09/553,431B

TIME: 15:03:51

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L:9 M:270 C: Current Application Number differs, Replaced Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date